



1

USF-T154X

SEQUENCE LISTING

<110> Laughran, Thomas
Kothapalli, Ravi

<120> Sphingosine 1-Phosphate Receptor Gene, SPPR

<130> USF-T154X

<140> US 10/024,019

<141> 2001-12-21

<150> US 60/257,119

<151> 2000-12-22

<160> 19

<170> PatentIn version 3.3

<210> 1

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe (see p. 8 of specification)

<400> 1

gcgcggccca tggagtc

17

<210> 2

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe (see p. 8 of specification)

<400> 2

cttttctgtg ttccaagca gaacgtcaat

30

<210> 3

<211> 398

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<223> Human sphingosine 1-Phosphate receptor (SPPR) amino acid sequence
(Figure 3)

<400> 3

Met Glu Ser Gly Leu Leu Arg Pro Ala Pro Val Ser Glu Val Ile Val
1 5 10 15

Leu His Tyr Asn Tyr Thr Gly Lys Leu Arg Gly Ala Arg Tyr Gln Pro
20 25 30

Gly Ala Gly Leu Arg Ala Asp Ala Val Val Cys Leu Ala Val Cys Ala
35 40 45

Phe Ile Val Leu Glu Asn Leu Ala Val Leu Leu Val Leu Gly Arg His
50 55 60

Pro Arg Phe His Ala Pro Met Phe Leu Leu Leu Gly Ser Leu Thr Leu
65 70 75 80

Ser Asp Leu Leu Ala Gly Ala Ala Tyr Ala Ala Asn Ile Leu Leu Ser
85 90 95

Gly Pro Leu Thr Leu Lys Leu Ser Pro Ala Leu Trp Phe Ala Arg Glu
100 105 110

Gly Gly Val Phe Val Ala Leu Thr Ala Ser Val Leu Ser Leu Leu Ala
115 120 125

Ile Ala Leu Glu Arg Ser Leu Thr Met Ala Arg Arg Gly Pro Ala Pro
130 135 140

Val Ser Ser Arg Gly Arg Thr Leu Ala Met Ala Ala Ala Ala Trp Gly
145 150 155 160

Val Ser Leu Leu Leu Gly Leu Leu Pro Ala Leu Gly Trp Asn Cys Leu
165 170 175

Gly Arg Leu Asp Ala Cys Ser Thr Val Leu Pro Leu Tyr Ala Lys Ala
180 185 190

Tyr Val Leu Phe Cys Val Leu Ala Phe Val Gly Ile Leu Ala Ala Ile
195 200 205

Cys Ala Leu Tyr Ala Arg Ile Tyr Cys Gln Val Arg Ala Asn Ala Arg
210 215 220

Arg Leu Pro Ala Arg Pro Gly Thr Ala Gly Thr Thr Ser Thr Arg Ala
 225 230 235 240

Arg Arg Lys Pro Arg Ser Leu Ala Leu Leu Arg Thr Leu Ser Val Val
 245 250 255

Leu Leu Ala Phe Val Ala Cys Trp Gly Pro Leu Phe Leu Leu Leu Leu
 260 265 270

Leu Asp Val Ala Cys Pro Ala Arg Thr Cys Pro Val Leu Leu Gln Ala
 275 280 285

Asp Pro Phe Leu Gly Leu Ala Met Ala Asn Ser Leu Leu Asn Pro Ile
 290 295 300

Ile Tyr Thr Leu Thr Asn Arg Asp Leu Arg His Ala Leu Leu Arg Leu
 305 310 315 320

Val Cys Cys Gly Arg His Ser Cys Gly Arg Asp Pro Ser Gly Ser Gln
 325 330 335

Gln Ser Ala Ser Ala Ala Glu Ala Ser Gly Gly Leu Arg Arg Cys Leu
 340 345 350

Pro Pro Gly Leu Asp Gly Ser Phe Ser Gly Ser Glu Arg Ser Ser Pro
 355 360 365

Gln Arg Asp Gly Leu Asp Thr Ser Gly Ser Thr Gly Ser Pro Gly Ala
 370 375 380

Pro Thr Ala Ala Arg Thr Leu Val Ser Glu Pro Ala Ala Asp
 385 390 395

<210> 4
 <211> 2336
 <212> DNA
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> Human sphingosine 1-Phosphate receptor (SPPR) cDNA sequence

(Figure 3)

<400> 4

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gccgacgcgg tgggtgtgct ggcggtgtgc gccttcacatg tgctagagaa tctagccgtg	180
ttgttggtgc tcggacgcca ccgcgccttc cacgctccca tgttcctgct cctgggcagc	240
ctcacgttgt cggatctgct ggcaggcgcc gcctacgcgg ccaacatcct actgtcgggg	300
ccgctcacgc tgaactgtc cccgcgcctc tggttcgac gggagggagg cgtcttcgtg	360
gcactcactg cgtccgtgct gagcctcctg gccatgcgcg tggagcgag cctcaccatg	420
gcgcgcaggg ggccgcgcgc cgtctccagt cgggggcgca cgctggcgat ggcagccgcg	480
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caggtaacgc ccaacgcgcg gcgcctgcgg gcaaggcccg ggactgcggg gaccacctcg	720
acccgggcgc gtcgaagcc gcgctcgctg gccttgctgc gcacgctcag cgtggtgctc	780
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cttgtgatgt gagctgagac ctctgtcctg ggaagaccaa aagaaaagca tttcaggatg	1560

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aggggaatggc atgcgcaaag gccctgagggc tgaaatgtgc ccatgtgttc taagaaatgc 1620
agcgaatgctg gtgtgcctgg agcaggggacg gaggggggaga atgggaggag acaaggagct 1680
gaaggagtag ttcccgaagg accttgtggg tgatatagag gacttcgctt ttgctctgag 1740
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acagggtgtct tgtggcctcc atgggaggtt gaaaaccaca gaagggtgaag gggggctgca 1860
ctgagccaca ggaacaatga tggagattcc agctaagccc agaccccgctg gattctagat 1920
agattttaga ggcagcagac agaattactg aggaattgag tgtaagagtg gaataaagtt 1980
atcaaggaca atgccaaagg tggggcaccc ccaaatttga ctttgggaga ctgagccaaa 2040
tcctatctgg taataaaatt tcttttttat ttttcttttc tttctttctt tctttctttc 2100
tttttttttt tttgagttgg gatcttgtgc tctgtcacc aggctggagt gcaatgggca 2160
caattatagc tcaactgcagc ctggaactcc tgggatcaag cctggagttc ctgcttcagc 2220
ctccctagta gctgggacta caggcatgca ccaccatgcc cagttaataa aatttcttca 2280
aatgcaaaaa aaaaaaaaaa aaaaaactcg aggggggggc cggtacccaa ttcgcc 2336

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<210> 5
<211> 400
<212> PRT
<213> Rattus norvegicus

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<220>
<221> MISC_FEATURE
<223> Nrg-1 rat genes (Figure 4)

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<400> 5

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Met Glu Ser Gly Leu Leu Arg Pro Ala Pro Val Ser Glu Val Ile Val
1           5           10           15

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Leu His Tyr Asn Tyr Thr Gly Lys Leu Arg Gly Ala Arg Tyr Gln Pro
          20           25           30

```

```

Gly Ala Gly Leu Arg Ala Asp Ala Ala Val Cys Leu Ala Val Cys Ala
          35           40           45

```

```

Phe Ile Val Leu Glu Asn Leu Ala Val Leu Leu Val Leu Gly Arg His
          50           55           60

```

Pro Arg Phe His Ala Pro Met Phe Leu Leu Leu Gly Ser Leu Thr Leu
65 70 75 80

Ser Asp Leu Leu Ala Gly Ala Ala Tyr Ala Thr Asn Ile Leu Leu Ser
85 90 95

Gly Pro Leu Thr Leu Arg Leu Ser Pro Ala Leu Trp Phe Ala Arg Glu
100 105 110

Gly Gly Val Phe Val Ala Leu Ala Ala Ser Val Leu Ser Leu Leu Ala
115 120 125

Ile Ala Ile Glu Arg His Leu Thr Met Ala Arg Arg Gly Pro Ala Pro
130 135 140

Ala Ala Ser Arg Ala Arg Thr Leu Ala Met Ala Val Ala Ala Trp Gly
145 150 155 160

Leu Leu Leu Thr Leu Gly Leu Leu Pro Ala Leu Gly Trp Asn Cys Leu
165 170 175

Gly Arg Leu Glu Ala Cys Ser Thr Val Leu Pro Val Tyr Ala Lys Ala
180 185 190

Tyr Val Leu Phe Cys Val Leu Ala Phe Leu Gly Ile Leu Ala Ala Ile
195 200 205

Cys Ala Leu Tyr Ala Arg Ile Tyr Cys Gln Val Arg Ala Asn Ala Arg
210 215 220

Arg Leu Arg Ala Gly Pro Gly Ser Arg Arg Ala Thr Ser Ser Ser Arg
225 230 235 240

Ser Arg His Thr Pro Arg Ser Leu Ala Leu Leu Arg Thr Leu Ser Val
245 250 255

Val Leu Leu Ala Phe Val Ala Cys Trp Gly Pro Leu Phe Leu Leu Leu
260 265 270

Leu Leu Asp Val Ala Cys Pro Ala Arg Ala Cys Pro Val Leu Leu Gln
275 280 285

Ala Asp Pro Phe Leu Gly Leu Ala Met Ala Asn Ser Leu Leu Asn Pro
 290 295 300

Ile Ile Tyr Thr Phe Thr Asn Arg Asp Leu Arg His Ala Leu Leu Arg
 305 310 315 320

Leu Leu Cys Cys Gly Arg Gly Pro Cys Asn Gln Asp Ser Ser Asn Ser
 325 330 335

Leu Gln Arg Ser Pro Ser Ala Val Gly Pro Ser Gly Gly Gly Leu Arg
 340 345 350

Arg Cys Leu Pro Pro Thr Leu Asp Arg Ser Ser Ser Pro Ser Glu His
 355 360 365

Ser Cys Pro Gln Arg Asp Gly Met Asp Thr Ser Cys Ser Thr Gly Ser
 370 375 380

Pro Gly Ala Ala Thr Ala Asn Arg Thr Leu Val Pro Asp Ala Thr Asp
 385 390 395 400

<210> 6
 <211> 400
 <212> PRT
 <213> Rattus norvegicus

<220>
 <221> MISC_FEATURE
 <223> EDG-8 rat genes (Figure 4)

<400> 6

Met Glu Ser Gly Leu Leu Arg Pro Ala Pro Val Ser Glu Val Ile Val
 1 5 10 15

Leu His Tyr Asn Tyr Thr Gly Lys Leu Arg Gly Ala Arg Tyr Gln Pro
 20 25 30

Gly Ala Gly Leu Arg Ala Asp Ala Ala Val Cys Leu Ala Val Cys Ala
 35 40 45

Phe Ile Val Leu Glu Asn Leu Ala Val Leu Leu Val Leu Gly Arg His
 50 55 60

Pro Arg Phe His Ala Pro Met Phe Leu Leu Leu Gly Ser Leu Thr Leu
65 70 75 80

Ser Asp Leu Leu Ala Gly Ala Ala Tyr Ala Thr Asn Ile Leu Leu Ser
85 90 95

Gly Pro Leu Thr Leu Arg Leu Ser Pro Ala Leu Trp Phe Ala Arg Glu
100 105 110

Gly Gly Val Phe Val Ala Leu Ala Ala Ser Val Leu Ser Leu Leu Ala
115 120 125

Ile Ala Leu Glu Arg His Leu Thr Met Ala Arg Arg Gly Pro Ala Pro
130 135 140

Ala Ala Ser Arg Ala Arg Thr Leu Ala Met Ala Val Ala Ala Trp Gly
145 150 155 160

Leu Ser Leu Leu Leu Gly Leu Leu Pro Ala Leu Gly Trp Asn Cys Leu
165 170 175

Gly Arg Leu Glu Ala Cys Ser Thr Val Leu Pro Leu Tyr Ala Lys Ala
180 185 190

Tyr Val Leu Phe Cys Val Leu Ala Phe Leu Gly Ile Leu Ala Ala Ile
195 200 205

Cys Ala Leu Tyr Ala Arg Ile Tyr Cys Gln Val Arg Ala Asn Ala Arg
210 215 220

Arg Leu Arg Ala Gly Pro Gly Ser Arg Arg Ala Thr Ser Ser Ser Arg
225 230 235 240

Ser Arg His Thr Pro Arg Ser Leu Ala Leu Leu Arg Thr Leu Ser Val
245 250 255

Val Leu Leu Ala Phe Val Ala Cys Trp Gly Pro Leu Phe Leu Leu Leu
260 265 270

Leu Leu Asp Val Ala Cys Pro Ala Arg Ala Cys Pro Val Leu Leu Gln

275

280

285

Ala Asp Pro Phe Leu Gly Leu Ala Met Ala Asn Ser Leu Leu Asn Pro
 290 295 300

Ile Ile Tyr Thr Phe Thr Asn Arg Asp Leu Arg His Ala Leu Leu Arg
 305 310 315 320

Leu Leu Cys Cys Gly Arg Gly Pro Cys Asn Gln Asp Ser Ser Asn Ser
 325 330 335

Leu Gln Arg Ser Pro Ser Ala Val Gly Pro Ser Gly Gly Gly Leu Arg
 340 345 350

Arg Cys Leu Pro Pro Thr Leu Asp Arg Ser Ser Ser Pro Ser Glu His
 355 360 365

Ser Cys Pro Gln Arg Asp Gly Met Asp Thr Ser Cys Ser Thr Gly Ser
 370 375 380

Pro Gly Ala Ala Thr Ala Asn Arg Thr Leu Val Pro Asp Ala Thr Asp
 385 390 395 400

<210> 7
 <211> 398
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> SPPR (Figure 4)

<400> 7

Met Glu Ser Gly Leu Leu Arg Pro Ala Pro Val Ser Glu Val Ile Val
 1 5 10 15

Leu His Tyr Asn Tyr Thr Gly Lys Leu Arg Gly Ala Arg Tyr Gln Pro
 20 25 30

Gly Ala Gly Leu Arg Ala Asp Ala Val Val Cys Leu Ala Val Cys Ala
 35 40 45

Phe Ile Val Leu Glu Asn Leu Ala Val Leu Leu Val Leu Gly Arg His
 50 55 60

Pro Arg Phe His Ala Pro Met Phe Leu Leu Leu Gly Ser Leu Thr Leu
 65 70 75 80

Ser Asp Leu Leu Ala Gly Ala Ala Tyr Ala Ala Asn Ile Leu Leu Ser
 85 90 95

Gly Pro Leu Thr Leu Lys Leu Ser Pro Ala Leu Trp Phe Ala Arg Glu
 100 105 110

Gly Gly Val Phe Val Ala Leu Thr Ala Ser Val Leu Ser Leu Leu Ala
 115 120 125

Ile Ala Leu Glu Arg Ser Leu Thr Met Ala Arg Arg Gly Pro Ala Pro
 130 135 140

Val Ser Ser Arg Gly Arg Thr Leu Ala Met Ala Ala Ala Ala Trp Gly
 145 150 155 160

Val Ser Leu Leu Leu Gly Leu Leu Pro Ala Leu Gly Trp Asn Cys Leu
 165 170 175

Gly Arg Leu Asp Ala Cys Ser Thr Val Leu Pro Leu Tyr Ala Lys Ala
 180 185 190

Tyr Val Leu Phe Cys Val Leu Ala Phe Val Gly Ile Leu Ala Ala Ile
 195 200 205

Cys Ala Leu Tyr Ala Arg Ile Tyr Cys Gln Val Arg Ala Asn Ala Arg
 210 215 220

Arg Leu Pro Ala Arg Pro Gly Thr Ala Gly Thr Thr Ser Thr Arg Ala
 225 230 235 240

Arg Arg Lys Pro Arg Ser Leu Ala Leu Leu Arg Thr Leu Ser Val Val
 245 250 255

Leu Leu Ala Phe Val Ala Cys Trp Gly Pro Leu Phe Leu Leu Leu Leu
 260 265 270

Leu Asp Val Ala Cys Pro Ala Arg Thr Cys Pro Val Leu Leu Gln Ala
 275 280 285

Asp Pro Phe Leu Gly Leu Ala Met Ala Asn Ser Leu Leu Asn Pro Ile
 290 295 300

Ile Tyr Thr Leu Thr Asn Arg Asp Leu Arg His Ala Leu Leu Arg Leu
 305 310 315 320

Val Cys Cys Gly Arg His Ser Cys Gly Arg Asp Pro Ser Gly Ser Gln
 325 330 335

Gln Ser Ala Ser Ala Ala Glu Ala Ser Gly Gly Leu Arg Arg Cys Leu
 340 345 350

Pro Pro Gly Leu Asp Gly Ser Phe Ser Gly Ser Glu Arg Ser Ser Pro
 355 360 365

Gln Arg Asp Gly Leu Asp Thr Ser Gly Ser Thr Gly Ser Pro Gly Ala
 370 375 380

Pro Thr Ala Ala Arg Thr Leu Val Ser Glu Pro Ala Ala Asp
 385 390 395

<210> 8
 <211> 254
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> Sphingosine-1- phosphate receptor.1 (Figure 5)

<400> 8

Met Glu Ser Gly Leu Leu Arg Pro Ala Pro Val Ser Glu Val Ile Val
 1 5 10 15

Leu His Tyr Asn Tyr Thr Gly Lys Leu Arg Gly Ala Arg Tyr Gln Pro
 20 25 30

Gly Ala Gly Leu Arg Ala Asp Ala Val Val Cys Leu Ala Val Cys Ala
 35 40 45

Phe Ile Val Leu Glu Asn Leu Ala Val Leu Leu Val Leu Gly Arg His
 50 55 60

Pro Arg Phe His Ala Pro Met Phe Leu Leu Leu Gly Ser Leu Thr Leu
 65 70 75 80

Ser Val Pro Ala Arg Pro Gly Thr Ala Gly Thr Thr Ser Thr Arg Ala
 85 90 95

Arg Arg Lys Pro Arg Ser Leu Ala Leu Leu Arg Thr Leu Ser Val Val
 100 105 110

Leu Leu Ala Phe Val Ala Cys Trp Gly Pro Leu Phe Leu Leu Leu Leu
 115 120 125

Leu Asp Val Ala Cys Pro Ala Arg Thr Cys Pro Val Leu Leu Gln Ala
 130 135 140

Asp Pro Phe Leu Gly Leu Ala Met Ala Asn Ser Leu Leu Asn Pro Ile
 145 150 155 160

Ile Tyr Thr Leu Thr Asn Arg Asp Leu Arg His Ala Leu Leu Arg Leu
 165 170 175

Val Cys Cys Gly Arg His Ser Cys Gly Arg Asp Pro Ser Gly Ser Gln
 180 185 190

Gln Ser Ala Ser Ala Ala Glu Ala Ser Gly Gly Leu Arg Arg Cys Leu
 195 200 205

Pro Pro Gly Leu Asp Gly Ser Phe Ser Gly Ser Glu Arg Ser Ser Pro
 210 215 220

Gln Arg Asp Gly Leu Asp Thr Ser Gly Ser Thr Gly Ser Pro Gly Ala
 225 230 235 240

Pro Thr Ala Ala Arg Thr Leu Val Ser Glu Pro Ala Ala Asp
 245 250

<210> 9

<211> 1698
 <212> DNA
 <213> Homo sapiens

<220>
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 <223> Sphingosine-1- phosphate receptor.1 (Figure 5)

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 cgccgacgcc gtggtgtgcc tggcggtgtg cgccttcata gtgctagaga atctagccgt 180
 gttgttggtg ctcggaacgcc acccgcgctt ccacgctccc atgttcctgc tcctgggcag 240
 cctcacgttg tcggtgcccg cacggccccg gactgcgggg accacctcga cccgggcgcg 300
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 cggctcggag cgctcatcgc cccagcgoga cgggctggac accagcggct ccacaggcag 720
 ccccggtgca cccacagccg cccggactct ggtatcagaa cgggctgcag actgacaccc 780
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 agctgagacc tctgtcctgg gaagacaaaa agaaaagcat ttcaggatga gggaatggca 1140
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 tcccgaagga ccttgtgggt gatatagagg acttcgcttt tgctctgagt gaggtgggag 1320
 ccatagaagc ttctaagcag aagagggact tgccctaatt caggtgatca caggtgtcct 1380

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gcagcagaca gaattactga ggaattgagt gtaagagtgg aataaagtta tcaaggacaa 1560
tgccaagggt ggggcacccc caaatgtgac tctgggagac tcagccaaat cctatctggt 1620
aataaaaattt ctttttttatt tttcttttct ttctttcttt cttttttttt tttttgagtt 1680
gggatcttgt gctctgtc 1698

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<210> 10
<211> 398
<212> PRT
<213> Homo sapiens

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<220>
<221> MISC_FEATURE
<223> Sphingosine-1- phosphate receptor (SIP) (Figures 14 and 15)

```

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<400> 10

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```

Met Glu Ser Gly Leu Leu Arg Pro Ala Pro Val Ser Glu Val Ile Val
1           5           10           15

```

```

Leu His Tyr Asn Tyr Thr Gly Lys Leu Arg Gly Ala Arg Tyr Gln Pro
          20           25           30

```

```

Gly Ala Gly Leu Arg Ala Asp Ala Val Val Cys Leu Ala Val Cys Ala
          35           40           45

```

```

Phe Ile Val Leu Glu Asn Leu Ala Val Leu Leu Val Leu Gly Arg His
          50           55           60

```

```

Pro Arg Phe His Ala Pro Met Phe Leu Leu Leu Gly Ser Leu Thr Leu
65           70           75           80

```

```

Ser Asp Leu Leu Ala Gly Ala Ala Tyr Ala Ala Asn Ile Leu Leu Ser
          85           90           95

```

```

Gly Pro Leu Thr Leu Lys Leu Ser Pro Ala Leu Trp Phe Ala Arg Glu
          100          105          110

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Gly Gly Val Phe Val Ala Leu Thr Ala Ser Val Leu Ser Leu Leu Ala

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115	120	125
Ile Ala Leu Glu Arg Ser Leu Thr Met Ala Arg Arg Gly Pro Ala Pro 130 135 140		
Val Ser Ser Arg Gly Arg Thr Leu Ala Met Ala Ala Ala Ala Trp Gly 145 150 155 160		
Val Ser Leu Leu Leu Gly Leu Leu Pro Ala Leu Gly Trp Asn Cys Leu 165 170 175		
Gly Arg Leu Asp Ala Cys Ser Thr Val Leu Pro Leu Tyr Ala Lys Ala 180 185 190		
Tyr Val Leu Phe Cys Val Leu Ala Phe Val Gly Ile Leu Ala Ala Ile 195 200 205		
Cys Ala Leu Tyr Ala Arg Ile Tyr Cys Gln Val Arg Ala Asn Ala Arg 210 215 220		
Arg Leu Pro Ala Arg Pro Gly Thr Ala Gly Thr Thr Ser Thr Arg Ala 225 230 235 240		
Arg Arg Lys Pro Arg Ser Leu Ala Leu Leu Arg Thr Leu Ser Val Val 245 250 255		
Leu Leu Ala Phe Val Ala Cys Trp Gly Pro Leu Phe Leu Leu Leu Leu 260 265 270		
Leu Asp Val Ala Cys Pro Ala Arg Thr Cys Pro Val Leu Leu Gln Ala 275 280 285		
Asp Pro Phe Leu Gly Leu Ala Met Ala Asn Ser Leu Leu Asn Pro Ile 290 295 300		
Ile Tyr Thr Leu Thr Asn Arg Asp Leu Arg His Ala Leu Leu Arg Leu 305 310 315 320		
Val Cys Cys Gly Arg His Ser Cys Gly Arg Asp Pro Ser Gly Ser Gln 325 330 335		

Gln Ser Ala Ser Ala Ala Glu Ala Ser Gly Gly Leu Arg Arg Cys Leu
 340 345 350

Pro Pro Gly Leu Asp Gly Ser Phe Ser Gly Ser Glu Arg Ser Ser Pro
 355 360 365

Gln Arg Asp Gly Leu Asp Thr Ser Gly Ser Thr Gly Ser Pro Gly Ala
 370 375 380

Pro Thr Ala Ala Arg Thr Leu Val Ser Glu Pro Ala Ala Asp
 385 390 395

<210> 11
 <211> 254
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> Sphingosine-1- phosphate receptor 1 (SIP1) (Figure 14)

<400> 11

Met Glu Ser Gly Leu Leu Arg Pro Ala Pro Val Ser Glu Val Ile Val
 1 5 10 15

Leu His Tyr Asn Tyr Thr Gly Lys Leu Arg Gly Ala Arg Tyr Gln Pro
 20 25 30

Gly Ala Gly Leu Arg Ala Asp Ala Val Val Cys Leu Ala Val Cys Ala
 35 40 45

Phe Ile Val Leu Glu Asn Leu Ala Val Leu Leu Val Leu Gly Arg His
 50 55 60

Pro Arg Phe His Ala Pro Met Phe Leu Leu Leu Gly Ser Leu Thr Leu
 65 70 75 80

Ser Val Pro Ala Arg Pro Gly Thr Ala Gly Thr Thr Ser Thr Arg Ala
 85 90 95

Arg Arg Lys Pro Arg Ser Leu Ala Leu Leu Arg Thr Leu Ser Val Val
 100 105 110

Leu Leu Ala Phe Val Ala Cys Trp Gly Pro Leu Phe Leu Leu Leu Leu
 115 120 125

Leu Asp Val Ala Cys Pro Ala Arg Thr Cys Pro Val Leu Leu Gln Ala
 130 135 140

Asp Pro Phe Leu Gly Leu Ala Met Ala Asn Ser Leu Leu Asn Pro Ile
 145 150 155 160

Ile Tyr Thr Leu Thr Asn Arg Asp Leu Arg His Ala Leu Leu Arg Leu
 165 170 175

Val Cys Cys Gly Arg His Ser Cys Gly Arg Asp Pro Ser Gly Ser Gln
 180 185 190

Gln Ser Ala Ser Ala Ala Glu Ala Ser Gly Gly Leu Arg Arg Cys Leu
 195 200 205

Pro Pro Gly Leu Asp Gly Ser Phe Ser Gly Ser Glu Arg Ser Ser Pro
 210 215 220

Gln Arg Asp Gly Leu Asp Thr Ser Gly Ser Thr Gly Ser Pro Gly Ala
 225 230 235 240

Pro Thr Ala Ala Arg Thr Leu Val Ser Glu Pro Ala Ala Asp
 245 250

<210> 12
 <211> 103
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> Sphingosine -1-Phosphate receptor 2 (Figure 6)

<400> 12

Met Glu Ser Gly Leu Leu Arg Pro Ala Pro Val Ser Glu Val Ile Val
 1 5 10 15

Leu His Tyr Asn Tyr Thr Gly Lys Leu Arg Gly Ala Arg Tyr Gln Pro
 20 25 30

Gly Ala Gly Leu Arg Ala Asp Ala Val Val Cys Leu Ala Val Cys Ala
 35 40 45

Phe Ile Val Leu Glu Asn Leu Ala Val Leu Leu Val Leu Gly Arg His
 50 55 60

Pro Arg Phe His Ala Pro Met Phe Leu Leu Leu Gly Ser Leu Thr Leu
 65 70 75 80

Ser Asp Leu Leu Ala Gly Ala Ala Tyr Ala Ala Ala Ala Arg Thr Leu
 85 90 95

Val Ser Glu Pro Ala Ala Asp
 100

<210> 13
 <211> 1245
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Sphingosine -1-Phosphate receptor 2 (Figure 6)

<400> 13
 cgcgcggccc atggagtcgg ggctgctgcg gccggcgccg gtgagcgagg tcatcgtcct 60
 gcattacaac tacaccggca agctccgcgg tgcgcgtac cagccgggtg ccggcctgcg 120
 cgcgcagccc gtggtgtgcc tggcgggtgtg cgccttcacg gtgctagaga atctagccgt 180
 gttgttggtg ctcgagccc acccgcgctt ccacgctccc atgttcctgc tcctgggcag 240
 cctcacgttg tcggatctgc tggcaggcgc cgcctacgcc gccgcgccc ggactctggt 300
 atcagaaccg gctgcagact gacaccctcg gccacgact gtcttcccaa gttttacaga 360
 cttgttcttt ttacataaag gaattttag gaaatgcagc caaaggtgca gtcggaaaag 420
 atgcagggga aatgtattta tgcagcgaca cccacaatg tgaacaaaca gacaaaaaat 480
 ctgtgccctc gtggaattga cgttctgctt gggaacacag aaaagaactc ggtgatgaaa 540
 taatggagat gattccagtg acaaacgaca gagatggtga tggtggtcag ggaagacctc 600
 tctgcagagg tagtgacttg tgatgtgagc tgagacctct gtctgggaa gacaaaaaga 660

```

aaagcatttc aggatgaggg aatggcatgc gcaaaggccc tgaggctgaa atgtgccat      720
gtgttctaag aaatgcagcg atgctggtgt gcctggagca gggacggagg gggagaatgg      780
gaggagacaa ggagctgaag gagtagttcc cgaaggacct tgtgggtgat atagaggact      840
tcgctttttgc tctgagttag gtgggagcca tagaagcttc taagcagaag agggacttgc      900
cctaattcag gtgatacacag gtgtottgtg gcctccatgg gaggttgaaa accagagaag      960
gtgaaggggg gctgcactga gccacaggaa caatgatgga gattccagct aagcccagac     1020
cccgtggatt ctagatagat tttagaggca gcagacagaa ttactgagga attgagtgtg     1080
agagtggaat aaagttatca aggacaatgc caaggggtggg gcacccccaa atttgactct     1140
gggagactca gccaaatcct atctggtaat aaaatttctt ttttattttt cttttctttc     1200
tttctttctt tttttttttt ttgagttggg atcttgtgct ctgtc                      1245

```

```

<210> 14
<211> 103
<212> PRT
<213> Homo sapiens

```

```

<220>
<221> MISC_FEATURE
<223> Sphingosine -1-Phosphate receptor 2 (SIP2) (Figure 15)

```

```

<400> 14

```

```

Met Glu Ser Gly Leu Leu Arg Pro Ala Pro Val Ser Glu Val Ile Val
1              5              10              15

```

```

Leu His Tyr Asn Tyr Thr Gly Lys Leu Arg Gly Ala Arg Tyr Gln Pro
              20              25              30

```

```

Gly Ala Gly Leu Arg Ala Asp Ala Val Val Cys Leu Ala Val Cys Ala
35              40              45

```

```

Phe Ile Val Leu Glu Asn Leu Ala Val Leu Leu Val Leu Gly Arg His
50              55              60

```

```

Pro Arg Phe His Ala Pro Met Phe Leu Leu Leu Gly Ser Leu Thr Leu
65              70              75              80

```

```

Ser Asp Leu Leu Ala Gly Ala Ala Tyr Ala Ala Ala Ala Arg Thr Leu
85              90              95

```

Val Ser Glu Pro Ala Ala Asp
100

<210> 15
<211> 2306
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Full-length (2.2 kb) nucleotide sequence of human S1P5 cDNA
(Figure 8)

```

<400> 15
gcgcggccca tggagtcggg gctgctgcgg ccggcgccgg tgagcgaggt catcgtcctg      60
cattacaact acaccggcaa gctccgcggt gcgcgctacc agccgggtgc cggcctgcgc      120
gccgacgccg tgggtgtgct ggcggtgtgc gccttcacgc tgctagagaa tctagccgtg      180
ttgttggtgc tcggacgcca ccgcgccttc cagcgtccca tgttcctgct cctgggcagc      240
ctcacgttgt cggatctgct ggcaggcgcc gcctacgcgc ccaacatcct actgtcgggg      300
ccgctcacgc tgaactgtc ccccgcgctc tggttcgcac gggagggagg cgtcttcgtg      360
gcactcactg cgtccgtgct gagcctcctg gccatcgcgc tggagcgag cctcaccatg      420
gcgcgcaggg ggcccgcgcc cgtctccagt cgggggcgca cgctggcgat ggcagccgcg      480
gcctggggcg tgctcgtgct cctcgggctc ctgccagcgc tgggctggaa ttgcctgggt      540
cgcttggaag cttgctccac tgtcttgccg ctctacgcca aggcctacgt gctcttctgc      600
gtgctcgctt tcgtgggcat cctggccgcg atctgtgcac tctacgcgcg catctactgc      660
caggtacgcg ccaacgcgcg gcgcctgccg gcacggcccg ggactgcggg gaccacctcg      720
acccggggcg gtcgcaagcc gcgctcgctg gccttgctgc gcacgctcag cgtggtgctc      780
ctggcctttg tggcatgttg gggccccctc ttctgctgc tgttgctcga cgtggcgtgc      840
ccggcgcgca cctgtcctgt actcctgcag gccgatccct tcctgggact ggccatggcc      900
aactcacttc tgaaccccat catctacacg ctcaccaacc gcgacctgcg ccacgcgctc      960
ctgcgccttg tctgctgcgg acgccactcc tgcggcagag acccgagtgg ctcccagcag     1020
tcggcgagcg cggctgaggc ttccgggggc ctgcgccgct gcctgcccc gggccttgat     1080
gggagcttca gcggctcgga gcgctcatcg ccccgcgcg acgggctgga caccagcggc     1140

```

```

tccacaggca gccccggtgc acccacagcc gcccggtctc tggatcaga accggctgca 1200
gactgacacc ctcggccac gactgtcttc ccaagtttta cagacttggt ctttttacat 1260
aaaggaattt gtaggaaatg cagccaaagg tgcagtcgga aaagatgcag gggaaatgta 1320
tttatgcagc gacacccac aatgtgaaca aacagacaaa aaatctgtgc cctcgtggaa 1380
ttgacgttct gcttggaac acagaaaaga actcgggtgat gaaataatgg agatgattcc 1440
agtgacaaac gacagagatg gtgatggtgg tcagggaaga cctctctgca gaggtagtga 1500
cttgtgatgt gagctgagac ctctgtcctg ggaagaccaa aagaaaagca tttcaggatg 1560
agggaatggc atgcgcaaag gccctgaggc tgaaatgtgc ccatgtgttc taagaaatgc 1620
agcgatgctg gtgtgcctgg agcagggacg gagggggaga atgggaggag acaaggagct 1680
gaaggagtag ttcccgaagg accttgtggg tgatatagag gacttcgctt ttgctctgag 1740
tgagggtgga gccatagaag cttctaagca gaagagggac ttgccctaat tcaggatgatc 1800
acagggtgtct tgtggcctcc atgggaggtt gaaaaccaca gaaggatgaag gggggctgca 1860
ctgagccaca ggaacaatga tggagattcc agctaagccc agaccccgctg gattctagat 1920
agattttaga ggcagcagac agaattactg aggaattgag tgtaagagtg gaataaagtt 1980
atcaaggaca atgccaaagg tggggcaccc ccaaatttga ctttgggaga ctacagccaaa 2040
tcctatctgg taataaaatt tcttttttat tttcttttc tttctttctt tctttctttc 2100
tttttttttt tttgagttgg gatcttgtgc tctgtcacc aggctggagt gcaatgggca 2160
caattatagc tactgcagc ctggaactcc tgggatcaag cctggagtgc ctgcttcagc 2220
ctccctagta gctgggacta caggcatgca ccaccatgcc cagttaataa aatttcttca 2280
aatgcaaaaa aaaaaaaaaa aaaaaa 2306

```

```

<210> 16
<211> 398
<212> PRT
<213> Homo sapiens

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```

<220>
<221> MISC_FEATURE
<223> Deduced amino acid sequence of human S1P5 cDNA coding region
      (Figure 8)

```

```

<400> 16

```

Met Glu Ser Gly Leu Leu Arg Pro Ala Pro Val Ser Glu Val Ile Val
 1 5 10 15

Leu His Tyr Asn Tyr Thr Gly Lys Leu Arg Gly Ala Arg Tyr Gln Pro
 20 25 30

Gly Ala Gly Leu Arg Ala Asp Ala Val Val Cys Leu Ala Val Cys Ala
 35 40 45

Phe Ile Val Leu Glu Asn Leu Ala Val Leu Leu Val Leu Gly Arg His
 50 55 60

Pro Arg Phe His Ala Pro Met Phe Leu Leu Leu Gly Ser Leu Thr Leu
 65 70 75 80

Ser Asp Leu Leu Ala Gly Ala Ala Tyr Ala Ala Asn Ile Leu Leu Ser
 85 90 95

Gly Pro Leu Thr Leu Lys Leu Ser Pro Ala Leu Trp Phe Ala Arg Glu
 100 105 110

Gly Gly Val Phe Val Ala Leu Thr Ala Ser Val Leu Ser Leu Leu Ala
 115 120 125

Ile Ala Leu Glu Arg Ser Leu Thr Met Ala Arg Arg Gly Pro Ala Pro
 130 135 140

Val Ser Ser Arg Gly Arg Thr Leu Ala Met Ala Ala Ala Ala Trp Gly
 145 150 155 160

Val Ser Leu Leu Leu Gly Leu Leu Pro Ala Leu Gly Trp Asn Cys Leu
 165 170 175

Gly Arg Leu Asp Ala Cys Ser Thr Val Leu Pro Leu Tyr Ala Lys Ala
 180 185 190

Tyr Val Leu Phe Cys Val Leu Ala Phe Val Gly Ile Leu Ala Ala Ile
 195 200 205

Cys Ala Leu Tyr Ala Arg Ile Tyr Cys Gln Val Arg Ala Asn Ala Arg
 210 215 220

Arg Leu Pro Ala Arg Pro Gly Thr Ala Gly Thr Thr Ser Thr Arg Ala
 225 230 235 240

Arg Arg Lys Pro Arg Ser Leu Ala Leu Leu Arg Thr Leu Ser Val Val
 245 250 255

Leu Leu Ala Phe Val Ala Cys Trp Gly Pro Leu Phe Leu Leu Leu Leu
 260 265 270

Leu Asp Val Ala Cys Pro Ala Arg Thr Cys Pro Val Leu Leu Gln Ala
 275 280 285

Asp Pro Phe Leu Gly Leu Ala Met Ala Asn Ser Leu Leu Asn Pro Ile
 290 295 300

Ile Tyr Thr Leu Thr Asn Arg Asp Leu Arg His Ala Leu Leu Arg Leu
 305 310 315 320

Val Cys Cys Gly Arg His Ser Cys Gly Arg Asp Pro Ser Gly Ser Gln
 325 330 335

Gln Ser Ala Ser Ala Ala Glu Ala Ser Gly Gly Leu Arg Arg Cys Leu
 340 345 350

Pro Pro Gly Leu Asp Gly Ser Phe Ser Gly Ser Glu Arg Ser Ser Pro
 355 360 365

Gln Arg Asp Gly Leu Asp Thr Ser Gly Ser Thr Gly Ser Pro Gly Ala
 370 375 380

Pro Thr Ala Ala Arg Thr Leu Val Ser Glu Pro Ala Ala Asp
 385 390 395

<210> 17
 <211> 398
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> Predicted amino acid sequence of S1P5 (Figures 12A and 12B)

<400> 17

Met Glu Ser Gly Leu Leu Arg Pro Ala Pro Val Ser Glu Val Ile Val
 1 5 10 15

Leu His Tyr Asn Tyr Thr Gly Lys Leu Arg Gly Ala Arg Tyr Gln Pro
 20 25 30

Gly Ala Gly Leu Arg Ala Asp Ala Val Val Cys Leu Ala Val Cys Ala
 35 40 45

Phe Ile Val Leu Glu Asn Leu Ala Val Leu Leu Val Leu Gly Arg His
 50 55 60

Pro Arg Phe His Ala Pro Met Phe Leu Leu Leu Gly Ser Leu Thr Leu
 65 70 75 80

Ser Asp Leu Leu Ala Gly Ala Ala Tyr Ala Ala Asn Ile Leu Leu Ser
 85 90 95

Gly Pro Leu Thr Leu Lys Leu Ser Pro Ala Leu Trp Phe Ala Arg Glu
 100 105 110

Gly Gly Val Phe Val Ala Leu Thr Ala Ser Val Leu Ser Leu Leu Ala
 115 120 125

Ile Ala Leu Glu Arg Ser Leu Thr Met Ala Arg Arg Gly Pro Ala Pro
 130 135 140

Val Ser Ser Arg Gly Arg Thr Leu Ala Met Ala Ala Ala Ala Trp Gly
 145 150 155 160

Val Ser Leu Leu Leu Gly Leu Leu Pro Ala Leu Gly Trp Asn Cys Leu
 165 170 175

Gly Arg Leu Asp Ala Cys Ser Thr Val Leu Pro Leu Tyr Ala Lys Ala
 180 185 190

Tyr Val Leu Phe Cys Val Leu Ala Phe Val Gly Ile Leu Ala Ala Ile
 195 200 205

Cys Ala Leu Tyr Ala Arg Ile Tyr Cys Gln Val Arg Ala Asn Ala Arg

210

215

220

Arg Leu Pro Ala Arg Pro Gly Thr Ala Gly Thr Thr Ser Thr Arg Ala
 225 230 235 240

Arg Arg Lys Pro Arg Ser Leu Ala Leu Leu Arg Thr Leu Ser Val Val
 245 250 255

Leu Leu Ala Phe Val Ala Cys Trp Gly Pro Leu Phe Leu Leu Leu Leu
 260 265 270

Leu Asp Val Ala Cys Pro Ala Arg Thr Cys Pro Val Leu Leu Gln Ala
 275 280 285

Asp Pro Phe Leu Gly Leu Ala Met Ala Asn Ser Leu Leu Asn Pro Ile
 290 295 300

Ile Tyr Thr Leu Thr Asn Arg Asp Leu Arg His Ala Leu Leu Arg Leu
 305 310 315 320

Val Cys Cys Gly Arg His Ser Cys Gly Arg Asp Pro Ser Gly Ser Gln
 325 330 335

Gln Ser Ala Ser Ala Ala Glu Ala Ser Gly Gly Leu Arg Arg Cys Leu
 340 345 350

Pro Pro Gly Leu Asp Gly Ser Phe Ser Gly Ser Glu Arg Ser Ser Pro
 355 360 365

Gln Arg Asp Gly Leu Asp Thr Ser Gly Ser Thr Gly Ser Pro Gly Ala
 370 375 380

Pro Thr Ala Ala Arg Thr Leu Val Ser Glu Pro Ala Ala Asp
 385 390 395

<210> 18
 <211> 254
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE

<223> Predicted amino acid sequence of S1P5-alpha (Figure 12A)

<400> 18

Met Glu Ser Gly Leu Leu Arg Pro Ala Pro Val Ser Glu Val Ile Val
1 5 10 15

Leu His Tyr Asn Tyr Thr Gly Lys Leu Arg Gly Ala Arg Tyr Gln Pro
20 25 30

Gly Ala Gly Leu Arg Ala Asp Ala Val Val Cys Leu Ala Val Cys Ala
35 40 45

Phe Ile Val Leu Glu Asn Leu Ala Val Leu Leu Val Leu Gly Arg His
50 55 60

Pro Arg Phe His Ala Pro Met Phe Leu Leu Leu Gly Ser Leu Thr Leu
65 70 75 80

Ser Val Pro Ala Arg Pro Gly Thr Ala Gly Thr Thr Ser Thr Arg Ala
85 90 95

Arg Arg Lys Pro Arg Ser Leu Ala Leu Leu Arg Thr Leu Ser Val Val
100 105 110

Leu Leu Ala Phe Val Ala Cys Trp Gly Pro Leu Phe Leu Leu Leu Leu
115 120 125

Leu Asp Val Ala Cys Pro Ala Arg Thr Cys Pro Val Leu Leu Gln Ala
130 135 140

Asp Pro Phe Leu Gly Leu Ala Met Ala Asn Ser Leu Leu Asn Pro Ile
145 150 155 160

Ile Tyr Thr Leu Thr Asn Arg Asp Leu Arg His Ala Leu Leu Arg Leu
165 170 175

Val Cys Cys Gly Arg His Ser Cys Gly Arg Asp Pro Ser Gly Ser Gln
180 185 190

Gln Ser Ala Ser Ala Ala Glu Ala Ser Gly Gly Leu Arg Arg Cys Leu
195 200 205

Pro Pro Gly Leu Asp Gly Ser Phe Ser Gly Ser Glu Arg Ser Ser Pro
 210 215 220

Gln Arg Asp Gly Leu Asp Thr Ser Gly Ser Thr Gly Ser Pro Gly Ala
 225 230 235 240

Pro Thr Ala Ala Arg Thr Leu Val Ser Glu Pro Ala Ala Asp
 245 250

<210> 19
 <211> 103
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> Predicted amino acid sequence of S1P5-beta (Figure 12B)

<400> 19

Met Glu Ser Gly Leu Leu Arg Pro Ala Pro Val Ser Glu Val Ile Val
 1 5 10 15

Leu His Tyr Asn Tyr Thr Gly Lys Leu Arg Gly Ala Arg Tyr Gln Pro
 20 25 30

Gly Ala Gly Leu Arg Ala Asp Ala Val Val Cys Leu Ala Val Cys Ala
 35 40 45

Phe Ile Val Leu Glu Asn Leu Ala Val Leu Leu Val Leu Gly Arg His
 50 55 60

Pro Arg Phe His Ala Pro Met Phe Leu Leu Leu Gly Ser Leu Thr Leu
 65 70 75 80

Ser Asp Leu Leu Ala Gly Ala Ala Tyr Ala Ala Ala Ala Arg Thr Leu
 85 90 95

Val Ser Glu Pro Ala Ala Asp
 100